STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/551,300_

Source: _IFWP_

Date Processed by STIC: _06/20/2006_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/551,300_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
   Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
   ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
   each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped
   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
   is Artificial Sequence. (see item 11 below)

11____Use of <220>   ~~Sequence(s)____missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use
   of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
   Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
   explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
   Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 06/20/2006
PATENT APPLICATION: US/10/551,300   TIME: 12:03:24

        Input Set : E:\SEQLIST.TXT
        Output Set: N:\CRF4\06202006\J551300.raw

     4 <110> APPLICANT: Trotta, Christopher R.
     6 <120> TITLE OF INVENTION: TARGETING ENZYMES OF THE tRNA SPLICING
     7   PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
     8   ANTI-PROLIFERATIVE MOLECULES
    10 <130> FILE REFERENCE: 10589-034-999
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/551,300
C--> 13 <141> CURRENT FILING DATE: 2005-09-27
    15 <150> PRIOR APPLICATION NUMBER: PCT/US2004/009590
    16 <151> PRIOR FILING DATE: 2004-03-26
    18 <150> PRIOR APPLICATION NUMBER: 60/458,067
    19 <151> PRIOR FILING DATE: 2003-03-27
    21 <160> NUMBER OF SEQ ID NOS: 4
    23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 465
    27 <212> TYPE: PRT
    28 <213> ORGANISM: Homo sapiens
    30 <220> FEATURE:
    31 <223> OTHER INFORMATION: HsSen2p
    33 <400> SEQUENCE: 1
    34 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
    35 1   5   10   15
    36 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
    37   20   25   30
    38 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
    39   35   40   45
    40 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
    41   50   55   60
    42 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
    43 65   70   75   80
    44 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
    45   85   90   95
    46 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
    47   100   105   110
    48 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
    49   115   120   125
    50 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
    51   130   135   140
    52 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
    53 145   150   155   160
    54 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
    55   165   170   175
    56 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys

```
57                180                   185                   190
58 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
59            195                   200                   205
60 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
61       210                   215                   220
62 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
63 225                   230                   235                   240
64 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
65                   245                   250                   255
66 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
67            260                   265                   270
68 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
69            275                   280                   285
70 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
71       290                   295                   300
72 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
73 305                   310                   315                   320
74 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
75                   325                   330                   335
76 Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
77            340                   345                   350
78 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
79            355                   360                   365
80 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
81       370                   375                   380
82 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
83 385                   390                   395                   400
84 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
85                   405                   410                   415
86 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
87            420                   425                   430
88 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
89            435                   440                   445
90 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
91       450                   455                   460
92 Leu
93 465
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 448
98 <212> TYPE: PRT
99 <213> ORGANISM: Homo sapiens
101 <220> FEATURE:
102 <223> OTHER INFORMATION: HsSen2 variant
104 <400> SEQUENCE: 2
105 Met Ala Glu Ala Val Phe His Ala Pro Lys Arg Lys Arg Arg Val Tyr
106 1               5                   10                  15
107 Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
108            20                  25                  30
109 Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
```

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110        35                   40                   45
111 Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
112        50                   55                   60
113 Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
114 65                   70                   75                   80
115 Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
116                  85                   90                   95
117 Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
118                  100                  105                  110
119 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
120        115                  120                  125
121 Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
122        130                  135                  140
123 Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
124 145                  150                  155                  160
125 Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
126                  165                  170                  175
127 Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
128                  180                  185                  190
129 Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
130        195                  200                  205
131 Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys
132        210                  215                  220
133 Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
134 225                  230                  235                  240
135 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
136                  245                  250                  255
137 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
138                  260                  265                  270
139 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
140        275                  280                  285
141 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Glu
142        290                  295                  300
143 Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln Pro
144 305                  310                  315                  320
145 Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys Gly
146                  325                  330                  335
147 Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu Tyr
148                  340                  345                  350
149 Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile Glu
150        355                  360                  365
151 Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser Trp
152        370                  375                  380
153 Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys Glu
154 385                  390                  395                  400
155 Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys Glu
156                  405                  410                  415
157 Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val Ile
158                  420                  425                  430
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163 <210> SEQ ID NO: 3
164 <211> LENGTH: 377
165 <212> TYPE: PRT
166 <213> ORGANISM: Saccharomyces cerevisiae
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Sc Sen2p
171 <400> SEQUENCE: 3
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173 1               5               10              15
174 Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu
175         20              25              30
176 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
177         35              40              45
178 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile
179         50              55              60
180 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
181 65              70              75              80
182 Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg
183             85              90              95
184 Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly
185             100             105             110
186 Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr
187         115             120             125
188 Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys
189     130             135             140
190 Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp
191 145             150             155             160
192 Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe
193             165             170             175
194 Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp
195             180             185             190
196 Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
197         195             200             205
198 Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu
199     210             215             220
200 Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
201 225             230             235             240
202 Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
203             245             250             255
204 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
205         260             265             270
206 Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
207         275             280             285
208 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
209     290             295             300
210 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
211 305             310             315             320
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RAW SEQUENCE LISTING   DATE: 06/20/2006
PATENT APPLICATION: US/10/551,300   TIME: 12:03:24

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Output Set: N:\CRF4\06202006\J551300.raw

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212 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu
213              325              330              335
214 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn
215              340              345              ·350
216 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys
217          355              360              365
218 Arg Trp Val Pro Gly Arg Asn Arg Asp
219     370              375
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 5
224 <212> TYPE: PRT
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Motif
230 <400> SEQUENCE: 4
231 Tyr Arg Gly Gly Tyr
232 1               5
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Invalid Response. What is the Source of genetic Material? Pls See Item # 11 on Error Summary (handwritten annotation)

VERIFICATION SUMMARY   DATE: 06/20/2006
PATENT APPLICATION: **US/10/551,300** TIME: 12:03:25

Input Set : **E:\SEQLIST.TXT**
Output Set: **N:\CRF4\06202006\J551300.raw**

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date